

OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 16:33:27 ; Search time 790.5 Seconds  
(without alignments)  
1900.205 Million cell updates/sec

Title: US-09-856-850A-1  
Perfect score: 31  
Sequence: 1 gaaacgaggatccatgctcaaaatcgccacc 31

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 14:50:22 ; Search time 200 Seconds  
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Title: US-09-856-850A-1  
Perfect score: 31  
Sequence: 1 gaaacgaggatccatgctcaaaatcgccacc 31

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
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## SUMMARIES

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 14:55:02 ; Search time 68.5 Seconds  
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Title: US-09-856-850A-1  
Perfect score: 31  
Sequence: 1 gaaacgaggatccatgctcaaaatcgccacc 31

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

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## SUMMARIES

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OM nucleic - nucleic search, using sw model

Run on: March 25, 2005, 16:47:32 ; Search time 230.5 Seconds  
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Title: US-09-856-850A-1  
Perfect score: 31  
Sequence: 1 gaaacgaggatccatgctcaaaatcgccacc 31

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

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Run on: March 25, 2005, 16:28:48 ; Search time 1405 Seconds  
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Title: US-09-856-850A-1  
Perfect score: 31  
Sequence: 1 gaaacgaggatccatgctcaaaatcgccacc 31

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
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3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
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Title: US-09-856-850A-2  
Perfect score: 31  
Sequence: 1 ttgtcactgcagctacacgtcaaacacagc 31

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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